

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 08/910, 449
Source: IFW16
Date Processed by STIC: 07/18/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/910,449

DATE: 07/18/2006

TIME: 10:52:33

Input Set : N:\Crif3\RULE60\08910449.RAW
 Output Set: N:\CRF4\07172006\H910449.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Alderson, Mark R.
 6 Goodwin, Raymond G.
 7 Smith, Craig A.
 9 (ii) TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
 11 (iii) NUMBER OF SEQUENCES: 18
 13 (iv) CORRESPONDENCE ADDRESS:
 14 (A) ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 15 (B) STREET: 51 University Street
 16 (C) CITY: Seattle
 17 (D) STATE: Washington
 18 (E) COUNTRY: US
 19 (F) ZIP: 98101
 21 (v) COMPUTER READABLE FORM:
 22 (A) MEDIUM TYPE: Floppy disk
 23 (B) COMPUTER: Apple Power Macintosh
 24 (C) OPERATING SYSTEM: Apple 7.5.3
 25 (D) SOFTWARE: Microsoft Word, Version #6.0.1
 27 (vi) CURRENT APPLICATION DATA:
 C--> 28 (A) APPLICATION NUMBER: US/08/910,449
 C--> 29 (B) FILING DATE: 05-Aug-1997
 W--> 30 (C) CLASSIFICATION: 435
 32 (vii) PRIOR APPLICATION DATA:
 33 (A) APPLICATION NUMBER: US/08/236,918
 34 (B) FILING DATE: 06-May-1994
 37 (A) APPLICATION NUMBER: US 08/060,843
 38 (B) FILING DATE: 07-May-1993
 42 (viii) ATTORNEY/AGENT INFORMATION:
 43 (A) NAME: Anderson, Kathryn A.
 44 (B) REGISTRATION NUMBER: 32,172
 45 (C) REFERENCE/DOCKET NUMBER: 2801-B
 47 (ix) TELECOMMUNICATION INFORMATION:
 48 (A) TELEPHONE: (206) 587-0430
 49 (B) TELEFAX: (206) 233-0644
 52 (2) INFORMATION FOR SEQ ID NO: 1:
 54 (i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 1254 base pairs
 56 (B) TYPE: nucleic acid
 57 (C) STRANDEDNESS: single
 58 (D) TOPOLOGY: linear
 60 (ii) MOLECULE TYPE: cDNA to mRNA
 62 (iii) HYPOTHETICAL: NO

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64      (iv) ANTI-SENSE: NO
67      (vii) IMMEDIATE SOURCE:
68          (B) CLONE: murine 4-1BB-L
70      (ix) FEATURE:
71          (A) NAME/KEY: CDS
72          (B) LOCATION: 53..979
75      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
77  AGCCTATAAA GCACGGGCAC TGGCGGGAGA CGTGCACTGA CCGACCGTGG TA ATG      55
78                                         Met
79                                         1
81  GAC CAG CAC ACA CTT GAT GTG GAG GAT ACC GCG GAT GCC AGA CAT CCA      103
82  Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His Pro
83              5              10              15
85  GCA GGT ACT TCG TGC CCC TCG GAT GCG GCG CTC CTC AGA GAT ACC GGG      151
86  Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr Gly
87      20              25              30
89  CTC CTC GCG GAC GCT GCG CTC CTC TCA GAT ACT GTG CGC CCC ACA AAT      199
90  Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr Asn
91      35              40              45
93  GCC GCG CTC CCC ACG GAT GCT GCC AAC CCT GCG GTT AAT GTT CGG GAT      247
94  Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg Asp
95  50              55              60              65
97  CGC GAG GCC GCG TGG CCG CCT GCA CTG AAC TTC TGT TCC CGC CAC CCA      295
98  Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His Pro
99      70              75              80
101 AAG CTC TAT GGC CTA GTC GCT TTG GTT TTG CTG CTT CTG ATC GCC GCC      343
102 Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Leu Ile Ala Ala
103      85              90              95
105 TGT GTT CCT ATC TTC ACC CGC ACC GAG CCT CGG CCA GCG CTC ACA ATC      391
106 Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile
107      100              105              110
109 ACC ACC TCG CCC AAC CTG GGT ACC CGA GAG AAT AAT GCA GAC CAG GTC      439
110 Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln Val
111      115              120              125
113 ACC CCT GTT TCC CAC ATT GGC TGC CCC AAC ACT ACA CAA CAG GGC TCT      487
114 Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly Ser
115 130              135              140              145
117 CCT GTG TTC GCC AAG CTA CTG GCT AAA AAC CAA GCA TCG TTG TGC AAT      535
118 Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys Asn
119      150              155              160
121 ACA ACT CTG AAC TGG CAC AGC CAA GAT GGA GCT GGG AGC TCA TAC CTA      583
122 Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu
123      165              170              175
125 TCT CAA GGT CTG AGG TAC GAA GAA GAC AAA AAG GAG TTG GTG GTA GAC      631
126 Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val Asp
127      180              185              190
129 AGT CCC GGG CTC TAC TAC GTA TTT TTG GAA CTG AAG CTC AGT CCA ACA      679
130 Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro Thr
131      195              200              205

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133 TTC ACA AAC ACA GGC CAC AAG GTG CAG GGC TGG GTC TCT CTT GTT TTG      727
134 Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val Leu
135 210      215      220      225
137 CAA GCA AAG CCT CAG GTA GAT GAC TTT GAC AAC TTG GCC CTG ACA GTG      775
138 Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr Val
139      230      235      240
141 GAA CTG TTC CCT TGC TCC ATG GAG AAC AAG TTA GTG GAC CGT TCC TGG      823
142 Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser Trp
143      245      250      255
145 AGT CAA CTG TTG CTC CTG AAG GCT GGC CAC CGC CTC AGT GTG GGT CTG      871
146 Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly Leu
147      260      265      270
149 AGG GCT TAT CTG CAT GGA GCC CAG GAT GCA TAC AGA GAC TGG GAG CTG      919
150 Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu
151      275      280      285
153 TCT TAT CCC AAC ACC ACC AGC TTT GGA CTC TTT CTT GTG AAA CCC GAC      967
154 Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro Asp
155 290      295      300      305
157 AAC CCA TCG GAA TGAGAACTAT CCTTCTGTG ACTCCTAGTT GCTAAGTCCT      1019
158 Asn Pro Trp Glu
161 CAAGCTGCTA TGTTTTATGG GGTCTGAGCA GGGGTCCCTT CCATGACTTT CTCTTGCTT      1079
163 TAACTGGACT TGGTATTAT TCTGAGCATA GCTCAGACAA GACTTTATAT AATTCAGTAG      1139
165 ATAGCATTAG TAACTGCTG GGCAGCTGCT AGATAAAAAA AAATTTCTAA ATCAAAGTTT      1199
167 ATATTTATAT TAATATATAA AAATAAATGT GTTTGTAAAT AAAAAAAAAA AAAAA      1254
170 (2) INFORMATION FOR SEQ ID NO: 2:
172 (i) SEQUENCE CHARACTERISTICS:
173 (A) LENGTH: 309 amino acids
174 (B) TYPE: amino acid
175 (D) TOPOLOGY: linear
177 (ii) MOLECULE TYPE: protein
179 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
181 Met Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His
182 1      5      10      15
184 Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr
185      20      25      30
187 Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr
188      35      40      45
190 Asn Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg
191      50      55      60
193 Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His
194 65      70      75      80
196 Pro Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Leu Ile Ala
197      85      90      95
199 Ala Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr
200      100      105      110
202 Ile Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln
203      115      120      125
205 Val Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly
206      130      135      140

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208 Ser Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys
209 145          150          155          160
211 Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr
212          165          170          175
214 Leu Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val
215          180          185          190
217 Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro
218 195          200          205
220 Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val
221 210          215          220
223 Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr
224 225          230          235          240
226 Val Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser
227          245          250          255
229 Trp Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly
230          260          265          270
232 Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu
233          275          280          285
235 Leu Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro
236 290          295          300
238 Asp Asn Pro Trp Glu
239 305
241 (2) INFORMATION FOR SEQ ID NO: 3:
243 (i) SEQUENCE CHARACTERISTICS:
244 (A) LENGTH: 1618 base pairs
245 (B) TYPE: nucleic acid
246 (C) STRANDEDNESS: single
247 (D) TOPOLOGY: linear
249 (ii) MOLECULE TYPE: cDNA to mRNA
251 (iii) HYPOTHETICAL: NO
253 (iv) ANTI-SENSE: NO
256 (vii) IMMEDIATE SOURCE:
257 (B) CLONE: human 4-1BB-L(7A)
259 (ix) FEATURE:
260 (A) NAME/KEY: CDS
261 (B) LOCATION: 4..765
264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
266 GTC ATG GAA TAC GCC TCT GAC GCT TCA CTG GAC CCC GAA GCC CCG TGG      48
267 Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp
268 1 5 10 15
270 CCT CCC GCG CCC CGC GCT CGC GCC TGC CGC GTA CTG CCT TGG GCC CTG      96
271 Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu
272 20 25 30
274 GTC GCG GGG CTG CTG CTG CTG CTG CTC GCT GCC GCC TGC GCC GTC      144
275 Val Ala Gly Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val
276 35 40 45
278 TTC CTC GCC TGC CCC TGG GCC GTG TCC GGG GCT CGC GCC TCG CCC GGC      192
279 Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly
280 50 55 60

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282	TCC	GCG	GCC	AGC	CCG	AGA	CTC	CGC	GAG	GGT	CCC	GAG	CTT	TCG	CCC	GAC	240
283	Ser	Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	
284	65						70					75					
286	GAT	CCC	GCC	GGC	CTC	TTG	GAC	CTG	CGG	CAG	GGC	ATG	TTT	GCG	CAG	CTG	288
287	Asp	Pro	Ala	Gly	Leu	Leu	Asp	Leu	Arg	Gln	Gly	Met	Phe	Ala	Gln	Leu	
288	80					85					90				95		
290	GTG	GCC	CAA	AAT	GTT	CTG	CTG	ATC	GAT	GGG	CCC	CTG	AGC	TGG	TAC	AGT	336
291	Val	Ala	Gln	Asn	Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser	Trp	Tyr	Ser	
292					100					105					110		
294	GAC	CCA	GGC	CTG	GCA	GGC	GTG	TCC	CTG	ACG	GGG	GGC	CTG	AGC	TAC	AAA	384
295	Asp	Pro	Gly	Leu	Ala	Gly	Val	Ser	Leu	Thr	Gly	Gly	Leu	Ser	Tyr	Lys	
296				115					120					125			
298	GAG	GAC	ACG	AAG	GAG	CTG	GTG	GTG	GCC	AAG	GCT	GGA	GTC	TAC	TAT	GTC	432
299	Glu	Asp	Thr	Lys	Glu	Leu	Val	Val	Ala	Lys	Ala	Gly	Val	Tyr	Tyr	Val	
300			130					135						140			
302	TTC	TTT	CAA	CTA	GAG	CTG	CGG	CGC	GTG	GTG	GCC	GGC	GAG	GGC	TCA	GGC	480
303	Phe	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly	
304		145					150					155					
306	TCC	GTT	TCA	CTT	GCG	CTG	CAC	CTG	CAG	CCA	CTG	CGC	TCT	GCT	GCT	GGG	528
307	Ser	Val	Ser	Leu	Ala	Leu	His	Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly	
308	160					165					170				175		
310	GCC	GCC	GCC	CTG	GCT	TTG	ACC	GTG	GAC	CTG	CCA	CCC	GCC	TCC	TCC	GAG	576
311	Ala	Ala	Ala	Leu	Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu	
312				180						185					190		
314	GCT	CGG	AAC	TCG	GCC	TTC	GGT	TTC	CAG	GGC	CGC	TTG	CTG	CAC	CTG	AGT	624
315	Ala	Arg	Asn	Ser	Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser	
316			195						200					205			
318	GCC	GGC	CAG	CGC	CTG	GGC	GTC	CAT	CTT	CAC	ACT	GAG	GCC	AGG	GCA	CGC	672
319	Ala	Gly	Gln	Arg	Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg	
320			210					215						220			
322	CAT	GCC	TGG	CAG	CTT	ACC	CAG	GGC	GCC	ACA	GTC	TTG	GGA	CTC	TTC	CGG	720
323	His	Ala	Trp	Gln	Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg	
324		225					230							235			
326	GTG	ACC	CCC	GAA	ATC	CCA	GCC	GGA	CTC	CCT	TCA	CCG	AGG	TCG	GAA		765
327	Val	Thr	Pro	Glu	Ile	Pro	Ala	Gly	Leu	Pro	Ser	Pro	Arg	Ser	Glu		
328	240					245					250						
330	AACGCCCAGC	CTGGGTGCAG	CCCACCTGGA	CAGAGTCCGA	ATCCTACTCC	ATCCTTCATG											825
332	GAGACCCCTG	GTGCTGGGTC	CCTGCTGCTT	TCTCTACCTC	AAGGGGCTTG	GCAGGGGTCC											885
334	CTGCTGCTGA	CCTCCCCTTG	AGGACCCTCC	TCACCCACTC	CTTCCCCAAG	TTGGACCTTG											945
336	ATATTTTATT	TGAGCCTGAG	CTCAGATAAT	ATATTATATA	TATTATATAT	ATATATATAT											1005
338	TTCTATTTAA	AGAGGATCCT	GAGTTTGTGA	ATGGACTTTT	TTAGAGGAGT	TGTTTTGGGG											1065
340	GGGGGGTCTT	CGACATTGCC	GAGGCTGGTC	TTGAACTCCT	GGACTTAGAC	GATCCTCCTG											1125
342	CCTCAGCCTC	CCAAGCAACT	GGGATTCATC	CTTTCTATTA	ATTCAATTGTA	CTTATTTGCC											1185
344	TATTTGTGTG	TATTGAGCAT	CTGTAATGTG	CCAGCATTGT	GCCCAGGCTA	GGGGGCTATA											1245
346	GAAACATCTA	GAAATAGACT	GAAAGAAAAT	CTGAGTTATG	GTAATACGTG	AGGAATTTAA											1305
348	AGACTCATCC	CCAGCCTCCA	CCTCCTGTGT	GATACTTGGG	GGCTAGCTTT	TTTCTTTCTT											1365
350	TCTTTTTTTT	GAGATGGTCT	TGTTCTGTCA	ACCAGGCTAG	AATGCAGCGG	TGCAATCATG											1425
352	AGTCAATGCA	GCCTCCAGCC	TCGACCTCCC	GAGGCTCAGG	TGATCCTCCC	ATCTCAGCCT											1485
354	CTCGAGTAGC	TGGGACCACA	GTTGTGTGCC	ACCACACTTG	GCTAACTTTT	TAATTTTTTTT											1545

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\08910449.RAW

Output Set: N:\CRF4\07172006\H910449.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:39 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)